

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 28, 2004, 17:42:42 ; Search time 1382.52 Seconds
(without alignments)
9232.292 Million cell updates/sec

Title: US-09-490-609b-280
Perfect score: 312
Sequence: 1 tcacaccacaggtgtgcatg.....aggctcatgtgtccaccatg 312

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenBml:.*
1: gb_ba:.*
2: gb_htg:.*
3: gb_in:.*
4: gb_ov:.*
5: gb_ov:.*
6: gb_pat:.*
7: gb_ph:.*
8: gb_pl:.*
9: gb_pr:.*
10: gb_ro:.*
11: gb_sts:.*
12: gb_sy:.*
13: gb_un:.*
14: gb_vl:.*
15: em_ba:.*
16: em_fun:.*
17: em_hum:.*
18: em_in:.*
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20: em_om:.*
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22: em_ov:.*
23: em_pat:.*
24: em_ph:.*
25: em_pl:.*
26: em_ro:.*
27: em_sts:.*
28: em_un:.*
29: em_vl:.*
30: em_htg_hum:.*
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32: em_htg_other:.*
33: em_htg_mus:.*
34: em_htg_pln:.*
35: em_htg_rtd:.*
36: em_htg_mam:.*
37: em_htg_vtl:.*
38: em_sy:.*
39: em_htgo_hum:.*
40: em_htgo_mus:.*
41: em_htgo_other:.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	299.4	96.0	1605	AB037934	AB037934 Rattus no
2	298.4	95.6	1594	10 R3C8P1	D38467 Rat mRNA fo
3	293.4	94.0	1594	10 R3C8P30A	X69021 R.norvegicu
4	285.4	91.5	1216	6 E09237	E09237 cDNA insert
5	216.8	69.5	1598	6 BC012710	BC012710 Mus muscu
6	214.8	68.8	1573	6 BD168858	BD168858 Senescen
7	214.8	68.8	1573	6 NMU28937	U28937 Mus musculu
8	190	60.9	1109	10 D6217	D6217 Mus musculu
9	184.2	59.0	400	10 D67071S2	D67068 Rat gene fo
10	184.2	59.0	260600	2 AC115307	AC115307 Rattus no
11	170.4	54.6	1375	9 AB028125	AB028125 Homo sapi
12	168.8	54.1	1356	6 AX409001	AX409001 Sequence
13	168.8	54.1	1356	6 BD079930	BD079930 Cancer-as
14	168.8	54.1	1356	6 E09013	E09013 cDNA encodi
15	168.8	54.1	1356	9 HUMSMP30	D31815 Human mRNA
16	168	53.8	1394	4 AB035446	AB035446 Bos tauru
17	160	51.3	1131	10 AB110216	AB110216 Mesocric
18	147.4	47.2	216812	10 AL672073	AL672073 Mouse sap
19	146.6	47.0	1438	9 AB032064	AB032064 Homo sapi
20	145.8	46.7	2280	10 MMU32170	U32170 Mus musculu
21	127	40.7	1357	4 AB035445	AB035445 Oryctolag
22	113	36.2	145456	9 AL513366	AL513366 Human DNA
23	97.6	31.3	1126	5 AB037936	AB037936 Xenopus 1
24	96	30.8	1088	5 AB033368	AB033368 Xenopus 1
25	95.2	30.5	1221	5 AB037935	AB037935 Gallus ga
26	77	24.7	867	10 D67071S1	D67071 Rat gene fo
27	57.4	18.4	142125	2 AC129835	AC129835 Canis fam
28	46.8	15.0	441	10 D67071S3	D67070 Rat gene fo
29	41	13.1	236629	9 AC120586	AC120586 Rattus no
30	41	13.1	280710	2 AC105612	AC105612 Rattus no
31	40.6	13.0	162509	2 AL137852	AL137852 Human DNA
32	39.6	12.7	36933	9 AC107074	AC107074 Homo sapi
33	38.4	12.3	176710	2 AC129434	AC129434 Rattus no
34	38.4	12.3	246362	2 AC111797	AC111797 Rattus no
35	37.2	11.9	229561	2 AC120067	AC120067 Rattus no
36	37	11.9	105087	9 AC093884	AC093884 Homo sapi
37	37	11.9	160196	2 AC016701	AC016701 Homo sapi
38	36.8	11.8	66619	2 AC100648	AC100648 Mus muscu
39	36.8	11.8	179705	10 AL627087	AL627087 Mouse DNA
40	36.8	11.8	181623	9 AL158071	AL158071 Human DNA
41	36.6	11.7	100562	9 AL355870	AL355870 Human DNA
42	36.4	11.7	153645	9 AC025426	AC025426 Homo sapi
43	36.4	11.7	175181	2 AC110529	AC110529 Mus muscu
44	36.4	11.7	183416	10 AL671269	AL671269 Mouse DNA
45	36.4	11.7	208700	2 AC140319	AC140319 Mus muscu

ALIGNMENTS

RESULT 1
AB037934 1605 bp mRNA linear ROD 09-FEB-2000
LOCUS AB037934
DEFINITION Rattus norvegicus mRNA for regucalcin, complete cde.
ACCESSION AB037934
VERSION AB037934.1 GI:6970312
KEYWORDS regucalcin.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
AUTHORS Misawa, H. and Yamaguchi, M.
TITLE The gene family encoding the calcium-binding protein regucalcin

Pred. No. is the number of results predicted by chance to have a

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1605)
AUTHORS Yamaguchi, M. and Misawa, H.
TITLE Direct Submission
JOURNAL Submitted (02-FEB-2000) Masayoshi Yamaguchi, Graduate School of

BASE COUNT	471 a	300 c	367 g	467 t
ORIGIN				

Query Match	96.0%	Score 299.4	DB 10	Length 1605
Best Local Similarity	99.4%	Pred. No. 2.9e-77		
Matches 311	Conservative	0	Mismatches 1	Indels 1

Qy	1	TTAACACCCAGTGTGGATGTGGAGTGTTCCTTTCCTTTCATTTTAAAGATATCTTG	60
Db	6	TTACACCCAGTGTGGATGTGGAGTGTTCCTTTCCTTTCATTTTAAAGATATCTTG	65
Qy	61	AAAAAAACCTGTCACTGTCTTTTCTCGACCAATGTCTTCCATCAAGATTGAATGTGT	120
Db	66	AAAAAAACCTGTCACTGTCTTTTCTCGACCAATGTCTTCCATCAAGATTGAATGTGT	125
Qy	121	TTAAGGGAGAACTACAGGTGTGGGGAGTCCCTGTGTGGAGAGAGCAATCAAAGTGTCTG	180
Db	126	TTAAGGGAGAACTACAGGTGTGGGGAGTCCCTGTGTGGAGAGAGCAATCAAAGTGTCTG	185
Qy	181	CTGTTTTGTAGACATCCCTTCAAAGACTGTCTCGATGGAGATTGGATCAGCAATCGAGTG	240
Db	186	CTGTTTTGTAGACATCCCTTCAAAGACTGTCTCGATGGAGATTGGATCAGCAATCGAGTG	245
Qy	241	CAGCGAGTGTGTGATGTATGCCCAAGTCAGTTCAGTGGACA-TTCGACAGTCAGAGAGCTAT	299
Db	246	CAGCGAGTGTGTGATGTATGCCCAAGTCAGTTCAGTGGACATTCGACAGTCAGAGAGCTAT	305
Qy	300	GTTCGCCACCATGG 312	
Db	306	GTTCGCCACCATGG 318	

RESULT 2	RATCBP1	1594 bp	mRNA	linear	ROD 08-FEB-1998
LOCUS	RATCBP1				
DEFINITION	Rat CBP1 for calcium-binding protein, complete cds.				
ACCESSION	D38467	D14327	D16386		
VERSION	D38467.1	GI:600378			
KEYWORDS	calcium-binding protein, regucalcin.				
SOURCE	Rattus norvegicus (Norway rat)				
ORGANISM	Rattus norvegicus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;				
	Rattus.				
REFERENCE	1 (sites)				
AUTHORS	Shimokawa, N. and Yamaguchi, M.				

TITLE	molecular cloning and sequencing of the cDNA coding for calcium-binding protein regucalcin from rat liver
JOURNAL	FEBS Lett. 327 (3), 251-255 (1993)
MEDLINE	93351639
PUBMED	8348951
REFERENCE	2 (bases 1 to 1594)
AUTHORS	Shimokawa,N. and Yamaguchi,M.
JOURNAL	Unpublished
COMMENT	On Dec 8, 1994 this sequence version replaced gi:391851.

FEATURES	location/Qualifiers
source	1..1594
	/organism="Rattus norvegicus"
	/mol_type="mRNA"
	/strain="Wistar"
	/db_xref="taxon:10116"
	/tissue_type="liver"
CDS	93..992

polysig	1154	.1158	
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ORIGIN			
Query Match	95.6%	Score 298.4	DB 10; Length 1594
Best Local Similarity	99.4%	Pred. No. 5.7e-77	
Matches 310; Conservative	0; Mismatches 1;	Indels 1;	Gaps 1;

Qy	2	TACAA	CCAGGTGGAGTGGAGGTGTTTCTTTGCTCTATTTAAAGATATCTGA	61
Db	1	TACAA	CCAGGTGGAGTGGAGGTGTTTCTTTGCTCTATTTAAAGATATCTGA	60
Qy	62	AAAAA	CCGTGCACTGCTCTTTCTCTGACCAATGTTCCATCAAGATGAATGTGTTT	121
Db	61	AAAAA	CCGTGCACTGCTCTTTCTCTGACCAATGTTCCATCAAGATGAATGTGTTT	120
Qy	122	TAA	GGAGAACTACAGGTGTGGGGAGTCCCCTGTGTGGAGAGGACATCAAAAGTCTGC	181
Db	121	TAA	GGAGAACTACAGGTGTGGGGAGTCCCCTGTGTGGAGAGGACATCAAAAGTCTGC	180
Qy	182	TGTTT	TAGACATCCCTTCAAAGACTGTCTGCCGATGGGATTCGATCAGCATATGAGTGC	241
Db	181	TGTTT	TAGACATCCCTTCAAAGACTGTCTGCCGATGGGATTCGATCAGCATATGAGTGC	240
Qy	242	AGC	AGTGTGTGTAGATATGCCCAATCAGTTCAGTGGCA-TTCGACATGCAGGAGGCTATG	300
Db	241	AGC	AGTGTGTGTAGATATGCCCAATCAGTTCAGTGGCACTTCGACAGTGCAGGAGGCTATG	300
Qy	301	TTG	CCACCATGG 312	
Db	301	TTG	CCACCATGG 312	

RESULT 3					
RNSMP30A					
LOCUS	RNSMP30A	1594 bp	mRNA	linear	ROD 16-NOV-1993
DEFINITION	R.norvegicus SMP30 mRNA for senescence marker protein-30.				
ACCESSION	X69021.1	X69021.1	GI:57254		
VERSION					

KEYWORDS senescence marker protein-30.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 1594)
AUTHORS Fujita,T., Shiraasawa,T., Uchida,K. and Maruyama,N.
TITLE Isolation of cDNA clone encoding rat senescence marker protein-30 (SMP30) and its tissue distribution
JOURNAL Biochim. Biophys. Acta 1132 (3), 297-305 (1992)
MEDLINE 93041931
PUBMED 1420310

REFERENCE 2 (bases 1 to 1594)
AUTHORS Fujita,T.
TITLE Direct Submision
JOURNAL Submitted (08-DEC-1992) T. Fujita, Dept. o Molecular Biology, Tokyo Metropolitan Inst. of Gerontology, 35-2, Sakaecho, Itabashi-Ku, Tokyo 173, JAPAN

FEATURES
source Location/Qualifiers
1..1594 /organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Wistar/Sic"
/db_xref="taxon:10116"
/dev_stage="6 months"
88..1588 /gene="SMP30"
88..987 /gene="SMP30"
/codon_start=1
/product="senescence marker protein-30"
/protein_id="CAA48786.1"
/db_xref="GI:57255"
/db_xref="SWISS-PROT:Q03336"
/translation="MSSIKIEVLRNRYRGESPVWEASKLLFVDIPSKTCVRMS ISNRVQVGVDAVSSVALROSGVATTGTKCALNWDOSVFILAMVDEKKNRF INDKVDPAGYFAGTAAETPAVLERRHGSLSLPDSVKYKFPQVVISGLDWSL DHKIFVYDLSLSTVDAPFDYDLPTGQISNRRTVYKMEKDEQIPDGCIDVEGLWVAC YNGRIVRIKIDPERGKRLQYKLPVDKTTSCCFGKRYSEMYTGCARDGSAEGLRQP DAQNIKFKITGLGVKGIAPYSYAG"

polya_signal 1148..1153 /gene="SMP30"
polya_signal 1566..1571 /gene="SMP30"
polya_site 1588 /gene="SMP30"
BASE COUNT 466 a 298 c 366 g 464 t
ORIGIN

Query Match 94.0%; Score 293.4; DB 10; Length 1594;
Best Local Similarity 99.3%; Pred. No. 1.7e-75;
Matches 305; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 7 CCCAGGTGAGTGTGAGTGTGCTTGTCTTCAATTTAAAGATCTTGAAGAAA 66
Db 1 CCAGGTGTGAGTGTGAGTGTGCTTGTCTTCAATTTAAAGATCTTGAAGAAA 60

QY 67 ACCTGTACTGTCTTCTTCTGCGACCATGTCTTCATCAAGATTGAATGTTTAAAG 126
Db 61 ACCTGTACTGTCTTCTTCTGCGACCATGTCTTCATCAAGATTGAATGTTTAAAG 120

QY 127 GAAACTACAGGTGTGGGAGTCCCTGTGTGGAGAGGACATCAAGTCTGCTGTTT 186
Db 121 GAAACTACAGGTGTGGGAGTCCCTGTGTGGAGAGGACATCAAGTCTGCTGTTT 180

QY 187 GTAGACATCCCTTCAAGACTGTCTGCGCATGGGATTCGATCAGCAATCAGTGCAGCGA 246
Db 181 GTAGACATCCCTTCAAGACTGTCTGCGCATGGGATTCGATCAGCAATCAGTGCAGCGA 240

QY 247 GTTGTGTATAGTCCCGCAGTCAAGTTCAGTGGCA-TTCGACAGTCAGGAGCTATGTTGCC 305
Db 241 GTTGTGTATAGTCCCGCAGTCAAGTTCAGTGGCA-TTCGACAGTCAGGAGCTATGTTGCC 300

QY 306 ACCATGG 312
Db 301 ACCATTG 307

RESULT 4
E09237
LOCUS E09237 1216 bp RNA linear PAT 29-SEP-1997
DEFINITION cDNA insert encoding Regucalcin.
ACCESSION E09237
VERSION E09237.1 GI:22025863
KEYWORDS JP 1995123985-A/1.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 1216)
AUTHORS Yamaguchi,M.
TITLE DNA FRAGMENT CODING FOR REGUCALCIN
JOURNAL Patent: JP 1995123985-A 1 16-MAY-1995;
YAMAGUCHI MASAYOSHI, DAI ICHI PURE CHEM CO LTD
COMMENT OS Rattus sp. (Rat)
PN JP 1995123985-A/1
PD 16-MAY-1995
PF 09-NOV-1993 JP 1993279349
PI YAMAGUCHI MASAYOSHI
PC C12N15/09,C12N1/21,C12N1/21,C12R1.19;
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FH source 1..1216 /organism="Rattus sp."
FT 80..979 /product="Regucalcin".
FT CDS /db_xref="taxon:10118"

FEATURES
source Location/Qualifiers
1..1216 /organism="Rattus sp."
/mol_type="genomic RNA"
/db_xref="taxon:10118"

BASE COUNT 338 a 231 c 309 g 338 t
ORIGIN

Query Match 91.5%; Score 285.4; DB 6; Length 1216;
Best Local Similarity 99.3%; Pred. No. 3.8e-73;
Matches 297; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 15 TGAATGCTGAGTGTGCTTGTCTTCAATTTAAAGATATCTTGAAGAAAACCTGTCA 74
Db 1 TGAATGCTGAGTGTGCTTGTCTTCAATTTAAAGATATCTTGAAGAAAACCTGTCA 60

QY 75 CTGTCTTCTTCTGCGACCATGTCTTCATCAAGATTGAATGTTTAAAGGAGAACTA 134
Db 61 CTGTCTTCTTCTGCGACCATGTCTTCATCAAGATTGAATGTTTAAAGGAGAACTA 120

QY 135 CAGGTGTGGAGTCCCTGTGTGGAGAGGACATCAAGTGTCTGCTTGTAGACT 194
Db 121 CAGGTGTGGAGTCCCTGTGTGGAGAGGACATCAAGTGTCTGCTTGTAGACT 180

QY 195 CCCTTCAAGACTGTCTGCGCATGGGATTCGATCAGCAATCAGTGCAGAGTGTGTGT 254
Db 181 CCCTTCAAGACTGTCTGCGCATGGGATTCGATCAGCAATCAGTGCAGAGTGTGTGT 240

QY 255 AGATGCCCGCAGTCAAGTTCAGTGGCA-TTCGACAGTCAGGAGCTATGTTGCCACCATGG 312
Db 241 AGATGCCCGCAGTCAAGTTCAGTGGCA-TTCGACAGTCAGGAGCTATGTTGCCACCATGG 299

RESULT 5
BC012710
LOCUS BC012710 1598 bp mRNA linear ROD 16-APR-2003

DEFINITION Mus musculus regucalcin, mRNA (cDNA clone MGC:14006 IMAGE:4210374), complete cds.

ACCESSION BC012710

VERSION BC012710.1 GI:15215230

KEYWORDS MGC.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 1598)

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Krausner R.D., Collins F.S., Wagner L., Steinem C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max A.S.I., Wang J., Hsieh F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schettz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez J., Helton E., Kettman M., Madan A., Rodriguez S., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Bicksteadt Y.S., Krzywinski M.I., Skalska U., Smalusz D.E., Schneringer A., Schein J.E., Jones S.J. and Marra M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

2 (bases 1 to 1598)

12477932

Strausberg R.

Direct Submission

Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

REMARK COMMENT

Contact: MGC help desk

Email: cgaps-rc@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

contact: amadan@systemsbiology.org

Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

FEATURES

source

1.1598

/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="MGC:14006 IMAGE:4210374"

/tissue_type="liver, normal, 5 month old male mouse."

/clone_id="NCI_CGAP_L19"

/lab_host="DHI0B"

/note="vector: pCMV-SPORT6"

1.1598

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/note="synonym: SMP30"

/db_xref="LocusID:19733"

/db_xref="MGI:108024"

CDS

86..985

/codon_start=1

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/protein_id="AAH12710.1"

/db_xref="GI:15215231"

/db_xref="LocusID:19733"

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BASE COUNT 466 a 293 c 370 g 469 t

ORIGIN

Query Match 69.5%; Score 216.8; DB 10; Length 1598;

Best Local Similarity 88.1%; Pred. No. 6.6e-53;

Matches 259; Conservative 0; Mismatches 32; Indels 3; Gaps 2;

QY 22 TGGAGTGTTCCTTTGCTCTCTATTATTTAAAGATATCTGAAAAAACCCTG-TCACTGTC 79

DB 12 TGGAGTGTTCCTTTGCTCTCTATTATTTAAAGATATCTGAAAAAACCCTGCACTGTC 71

QY 80 CTTTTCCTGCGACCAATGCTCTTCCATCAAGATTGAATGCTTTTAAAGGAGAACTACAGGT 139

DB 72 CTTTTCCTGTCACATGCTCTTCCATCAAGATTGAATGCTTTTAAAGGAGAACTACAGGT 131

QY 140 GTGGGAGTCCCTGCTGTGAGAGAGAGCATCAAGTGTCTGTTTGTAGACATCCCTT 199

DB 132 GTGGGAGTCTCTCTGTATGAGAGAGAGCATCAAGTGTCTGTTTGTAGATCCCTT 191

QY 200 CAAAGACTGTCTGCCGATGGATTCGATCGAATCGATGAGCGAGTGTGTAGATG 259

DB 192 CAAAGATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 251

QY 260 CCCCAGTCACTTCAGTGGCA-TTCGACAGTCAGAGGCTATGTTCCACCATG 312

DB 252 CCCCAGTCACTTCAGTGGCA-TTCGACAGTGTGAGGCTATGTTCCACCATG 305

RESULT 6

BD168858

LOCUS 1573 bp DNA linear PAT 17-JAN-2003

DEFINITION Senseless marker protein 30-deficient non-human animal, antibody

ACCESSION BD168858

VERSION WO 0234041-A/1

KEYWORDS WO 0234041-A/1

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1573)

Maruyama N. and Kasahara Y.

Senseless marker protein 30-deficient non-human animal, antibody

and method of constructing the same

Patent: WO 0234041-A 1 02-MAY-2002;

NAOKI MARUYAMA, YASUSHI KASAHARA

JOURNAL

OS Mus musculus (mouse)

PN WO 0234041-A/1

PD 02-MAY-2002

PF 22-OCT-2001 WO 2001JP009243

PR 23-OCT-2000 JP 00P 322234

PI NAOKI MARUYAMA, YASUSHI KASAHARA

PC A01K67/027, C12N15/12, C07K14/47, C12P21/08, C12N15/06 CC

Senseless marker protein 30-deficient non-human animal, CC

antibody and

CC method of constructing the same

FH Key location/Qualifiers

FT source 1.1573

FEATURES

source

1.1573

/organism="Mus musculus (mouse)"

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BASE COUNT      453 a      288 c      366 g      466 t
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Query Match      68.8%; Score 214.8; DB 6; Length 1573;
Best Local Similarity 88.0%; Pred. No. 2.6e-52;
Matches 257; Conservative 0; Mismatches 32; Indels 3; Gaps 2;

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DB 1  GAGTTTTCCTTGTCTTCTATTTTAAAGATATCTGAAAAAAGCTGCTCT 60
    |||
QY 82 TTTCCTGCACCATGCTCTTCATCATGATTGAATGTTTAAAGAGAACTACAGGTGT 141
    |||
DB 61 TTTCCTGTACCATGCTCTTCATCAAGTTGAATGTTTAAAGAGAACTACAGGTGT 120
    |||
QY 142 GGGAGTCCCTGTGTGGAGAGAGCATCAAGTGTCTGCTTTTGTAGACATCCCTTCA 201
    |||
DB 121 GGGAGTCTCCTGTATGGAGAGAGCATCAAGTGTCTGCTTTTGTAGATCCCTTCA 180
    |||
QY 202 AAGACTGTCTGCCGATGGGATTCGATCAGAACTGAGTGCAGAGAGTGTGTAATGCC 261
    |||
DB 181 AAGATTATTGTTCGATGGATGATGATGATGATGATGATGATGATGATGATGATGCC 240
    |||
QY 262 CCAGTCAGTTCAGTGGA--TTGACAGTCAGAGAGGCTATGTTGCCACCATGG 312
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DB 241 CCAGTCAGTTCAGTGGA--TTGACAGTCAGAGAGGCTATGTTGCCACCATGG 292
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RESULT 7
MMU28937      1573 bp      mRNA      linear      ROD 22-AUG-1996
LOCUS      Mus musculus senescence marker protein-30 (SMP30) mRNA, complete
DEFINITION      cds.
ACCESSION      U28937
VERSION      U28937.1
KEYWORDS      GI:1143999
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE      Fukuyama, T. and Maruyama, N.
AUTHORS      Fujita, T., Shirasawa, T. and Maruyama, N.
TITLE      Isolation and characterization of genomic and cDNA clones encoding
JOURNAL      mouse senescence marker protein-30 (SMP30)
MEDLINE      96328264
PUBMED      8765750
REFERENCE      2 (bases 1 to 1573)
AUTHORS      Shirasawa, T.
TITLE      Direct Submision
JOURNAL      Submitted (10-JUN-1995) Takuji Shirasawa, Molecular Pathology,
MEDLINE      Tokyo Metropolitan Institute of Gerontology, 35-2, Sakaecho,
PUBMED      Itabashi-ku, Tokyo 173, Japan
FEATURES
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        1..1573
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            /mol_type="mRNA"
            /strain="C57Black/6"
            /db_xref="taxon:10090"
            /tissue_type="liver"
            /dev_stage="adult"
            1..1573
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            73..972
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CDS
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polyA_signal
polyA_signal
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Query Match      68.8%; Score 214.8; DB 10; Length 1573;
Best Local Similarity 88.0%; Pred. No. 2.6e-52;
Matches 257; Conservative 0; Mismatches 32; Indels 3; Gaps 2;

QY 24 GAGTGTTCCTTGTCTTCTATTTTAAAGATATCTGAAAAAAGCTG--TCACGTCTCT 81
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DB 1  GAGTTTTCCTTGTCTTCTATTTTAAAGATATCTGAAAAAAGCTGCTCT 60
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QY 82 TTTCCTGCACCATGCTCTTCATCATGATTGAATGTTTAAAGAGAACTACAGGTGT 141
    |||
DB 61 TTTCCTGTACCATGCTCTTCATCAAGTTGAATGTTTAAAGAGAACTACAGGTGT 120
    |||
QY 142 GGGAGTCCCTGTGTGGAGAGAGCATCAAGTGTCTGCTTTTGTAGACATCCCTTCA 201
    |||
DB 121 GGGAGTCTCCTGTATGGAGAGAGCATCAAGTGTCTGCTTTTGTAGATCCCTTCA 180
    |||
QY 202 AAGACTGTCTGCCGATGGGATTCGATCAGAACTGAGTGCAGAGAGTGTGTAATGCC 261
    |||
DB 181 AAGATTATTGTTCGATGGATGATGATGATGATGATGATGATGATGATGATGATGCC 240
    |||
QY 262 CCAGTCAGTTCAGTGGA--TTGACAGTCAGAGAGGCTATGTTGCCACCATGG 312
    |||
DB 241 CCAGTCAGTTCAGTGGA--TTGACAGTCAGAGAGGCTATGTTGCCACCATGG 292
    |||

RESULT 8
D86217      1109 bp      mRNA      linear      ROD 07-FEB-1999
LOCUS      Mus musculus mRNA for regucalcin, complete cds.
DEFINITION      D86217
ACCESSION      D86217
VERSION      D86217.1
KEYWORDS      GI:1483151
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE      Fukuyama, T. and Yamaguchi, M.
AUTHORS      Murata, T. and Yamaguchi, M.
TITLE      Molecular cloning of the cDNA coding for regucalcin and its mRNA
JOURNAL      expression in mouse liver: the expression is stimulated by calcium
MEDLINE      administration
PUBMED      97422495
REFERENCE      2 (bases 1 to 1109)
AUTHORS      Yamaguchi, M.
TITLE      Direct Submision
JOURNAL      Submitted (24-JUN-1996) Masayoshi Yamaguchi, University of
MEDLINE      Shinzoku, Laboratory of Endocrinology and Molecular Metabolism,
PUBMED      Graduate School of Nutritional Sciences, 52-1 Yada, Shinzoku,
          Shinzoku 422, Japan (Tel:054-264-5580, Fax:054-264-5580)
COMMENT      Sequence updated (15-Jul-1996) by: Masayoshi Yamaguchi.
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 DKHIFYYIDSLSTTVDAFYDIDTQGISNRRIYVKKKEDQIPDGCITAEKGLWAC
 YNGRVRIDPETERLQIVKLPVDKITSCFFGGKDYSEMYTCARDGNABGLKOP
 DANGIFKIGLVGVGIAPYSYAG"

BASE COUNT 305 a 207 c 282 g 315 t

ORIGIN

Query Match 60.9%; Score 190; DB 10; Length 1109;
 Best Local Similarity 89.3%; Pred. No. 5.3e-45;
 Matches 216; Conservative 0; Mismatches 25; Indels 1; Gaps 1;

QY 72 TCACGTGCTTTCCGCGACCATGCTTCATCAAGATGAAGTGTAAAGGAGAA 131
 DB 3 TCACGTGCTTTCCGCGACCATGCTTCATCAAGATGAAGTGTAAAGGAGAA 62
 QY 132 CTACAGGTGGGAGAGTCCCTGTGTGGAGAGGAGCATCAAGTGTCTGTTTGTAGA 191
 DB 63 CTACAGGTGGGAGAGTCCCTGTGTGGAGAGGAGCATCAAGTGTCTGTTTGTAGA 122
 QY 192 CATCCCTTCAAAGACTGTCTGCCGATGGGATTGATGACATCGAGTGCAGAGTTGG 251
 DB 123 TATCCCTTCAAAGACTGTCTGCCGATGGGATTGATGACATCGAGTGCAGAGTTGG 182
 QY 252 TGTAGATGCCCCAGTGCAGTTCAGTGGCA-TTCGACAGTGCAGAGGCTATGTGCCACCAT 310
 DB 183 TGTAGATGCCCCAGTGCAGTTCAGTGGCA-TTCGACAGTGCAGAGGCTATGTGCCACCAT 242
 QY 311 GG 312
 DB 243 TG 244

RESULT 9
 LOCUS D67071S2 400 bp DNA linear ROD 14-Apr-2000
 DEFINITION Rat gene for regucalcin, exon2.
 ACCESSION D67069
 VERSION D67069.1 GI:1015329
 KEYWORDS regucalcin.
 SEGMENT 2 of 3
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1
 Yamaguchi, M., Makino, R. and Shimokawa, N.
 The 5' end sequences and exon organization in rat regucalcin gene
 JOURNAL Mol. Cell. Biochem. 165 (2), 145-150 (1996)
 MEDLINE 97133868
 PUBMED 8979263
 REFERENCES 2 (bases 1 to 400)
 YAMAGUCHI, M., MAKINO, R. and SHIMOKAWA, N.
 Characterization of the 5' end sequences and exon organization in
 rat regucalcin gene
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 400)
 YAMAGUCHI, M.
 Direct Submission
 JOURNAL Submitted (27-SEP-1995) Masayoshi Yamaguchi, Graduate School of
 Nutritional Sciences, University of Shizuoka, Laboratory of
 Metabolism and Endocrinology; 52-1 Yada, Shizuoka, Shizuoka 422,
 Japan (Tel:054-264-5580, Fax:054-264-5580)
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 129..144
 308..>400
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BASE COUNT 82 a 89 c 101 g 128 t

ORIGIN

Query Match 59.0%; Score 184.2; DB 10; Length 400;
 Best Local Similarity 91.5%; Pred. No. 2.6e-43;
 Matches 195; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 70 TGTCACTGCTTTTCTTCCGACCATGCTTCATCAAGATGAAGTGTAAAGGAG 129
 DB 121 TGTCTCAGTCCCTTTCCTGCGACCATGCTTCATCAAGATGAAGTGTAAAGGAG 180
 QY 130 AACTACAGGTGGGAGAGTCCCTGTGTGGAGAGGAGCATCAAGTGTCTGTTTGTAGA 189
 DB 181 AACTACAGGTGGGAGAGTCCCTGTGTGGAGAGGAGCATCAAGTGTCTGTTTGTAGA 240
 QY 190 GACATCCCTTCAAAGACTGTCTGCCGATGGGATTGATGACATCGAGTGCAGAGTT 249
 DB 241 GACATCCCTTCAAAGACTGTCTGCCGATGGGATTGATGACATCGAGTGCAGAGTT 300
 QY 250 GGTTGTAGATGCCCGAGTCAAGTTCAGTGGCATTC 282
 DB 301 GGTTGTAGATGCCCGAGTCAAGTTCAGTGGCATTC 333

RESULT 10
 LOCUS AC115307 260600 bp DNA linear HTG 09-NOV-2002
 DEFINITION Rattus norvegicus clone CH230-11F18, WORKING DRAFT SEQUENCE.
 ACCESSION AC115307
 VERSION AC115307.4 GI:24817861
 KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE Rattus norvegicus
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 260600)
 Muzny, D., Marie, Metzger, M., Lee, A., Abramson, S., Adams, C., Alder, J.,
 Allen, C., Allen, H., Alsbrooks, S., Amth, A., Anguiano, D.,
 Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
 Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
 Bissalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
 Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
 Cardenas, V., Carter, K., Cavazos, I., Ceaser, H., Cencer, A.,
 Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
 Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
 Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
 Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
 Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
 Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,
 Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
 Frazer, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
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 Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
 Kows, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
 Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
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Mawhinney, S., McLeod, M. P., McNeill, T. Z., Meenen, E.,
Milosavljevic, A., Miner, G., Minji, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Mundasa, M., Murphy, M., Natir, L.,
Narkaveis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nwokilemeh, O., Okwuon, G., Olariupagsoon, A., Pal, S., Parks, K.,
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Plopper, F., Poidexter, A., Popovic, D., Primus, E., Pu, L.-L.,
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Rives, C., Rodkey, T., Rojars, A., Rose, M., Rose, R., Ruit, S. J.,
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Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Sneed, A., Sodergren, E., Song, K.-Z., Soreiller, R., Sosa, J.,
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Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Valas, R., Vera, V., Villasa, D., Waldron, L., Walker, B., Wang, J.,
Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Williams, G., Willson, R., Wiczycki, R., Wooden, H., Worley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Medenhausen, A., Weiss, R., Smith, D. R., Holt, R.A., Smith, H. O.,
Weinstock, G. and Gibbs, R. A.

Direct Submission
Unpublished
2 (bases 1 to 260600)
Worley, K. C.

Direct Submission
Submitted (17-MAR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 260600)
Baylor College of Medicine

Rat Genome Sequencing Consortium.

Direct Submission
Submitted (09-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

On Nov 9, 2002 this sequence version replaced gi:22772493.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atilas
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GEBE
Center clone name: CH230-11F18
----- Summary Statistics
Assembly program: Phrap, version 0.990329
Consensus quality: 229014 bases at least Q40
Consensus quality: 231787 bases at least Q30
Consensus quality: 232904 bases at least Q20
Estimated insert size: 237320, sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* ([see \[http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html\]\(http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html\)](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have

FEATURES		source	
<p>* Provided by the submittor. * This sequence will be replaced * by the finished sequence as soon as it is available and * the accession number will be previewed. * 1 260600: contig of 260600 bp in length. Location/Qualifiers 1..260600 /organism="Rattus norvegicus" /mol_type="genomic DNA" /db_xref="taxon:10116" /clone="CH230-11F18" 1..2114 /note="wgs_end_extension clone_end:T7" 6641..7491 /note="clone_boundary clone_end:T7 site:ECORI end_sequence="BH340447" 88160..195463 /note="clone_boundary clone_end:Sp6 site:ECORI end_sequence="BH340449" 258937..260600 /note="wgs_end_extension clone_end:Sp6"</p>			
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Best Local Similarity	91.5%; Pred. NO. 3e-43;		
Matches 195; Conservative	0; Mismatches 18; Indels 0; Gaps 0;		
QY	70	TGTCACGTGCTCTTCCCTGCGACCAATGCTTCATCAAGATTGAATGTTTAAAGGAG	129
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QY	130	AACACAGGTGTGGGAGATCCCTGTGTGTGGAGAGGACATCAAAAGTGTCTGCTGTTGTA	189
DB	95022	AACACAGGTGTGGGAGATCCCTGTGTGTGGAGAGGACATCAAAAGTGTCTGCTGTTGTA	95081
QY	190	GACATCCCTTCAAGAGCTGTCTGCGCATGGGATTGCATACGCAATGAGTGCAGCGAGTT	249
DB	95082	GACATCCCTTCAAGAGCTGTCTGCGCATGGGATTGCATACGCAATGAGTGCAGCGAGTT	95144
QY	250	GGGTAGATGCCCAAGTCAGTTCAGTGGCATTC	282
DB	95142	GGGTAGATGCCCAAGTCAGTTCAGTGGCATTC	95174
RESULT 11			
LOCUS	AB028125	1375 bp	mRNA linear PRI 18-JUL-2000
DEFINITION	Homo sapiens mRNA for regucalcin, complete cds.		
ACCESSION	AB028125		
VERSION	AB028125.1	GI:5030903	
KEYWORDS	regucalcin.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	Misawa,H. and Yamaguchi,M.		
TITLE	Transcript heterogeneity of the human gene for Ca2+-binding protein regucalcin		
JOURNAL	Int. J. Mol. Med. 5 (3), 283-287 (2000)		
MEDLINE	20144201		
PUBMED	10677570		
REFERENCE	2 (bases 1 to 1375)		
AUTHORS	Yamaguchi,M. and Misawa,H.		
TITLE	Direct Submission		
JOURNAL	Submitted (31-MAY-1999) Masayoshi Yamaguchi, Graduate School of		

Nutritional Sciences, University of Shizuoka, Laboratory of Endocrinology and Molecular Metabolism, Yada 52-1, Shizuoka 422-8526, Japan (E-mail: yamaguchi@u-shizuoka-ken.ac.jp, Tel: +81-54-264-5580, Fax: +81-54-264-5580)

FEATURES

source

1.1375
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CDS

BASE COUNT 392 a 274 c 343 g 366 t
ORIGIN

Query Match 54.6%; Score 170.4; DB 9; Length 1375;
Best Local Similarity 76.3%; Pred. No. 3.2e-39;
Matches 235; Conservative 0; Mismatches 71; Indels 2; Gaps 2;

QY 6 ACCAGGTGTGATGCTGGAGTGTTCCTTCTCTATTTTAAAGATCTTGAAGA 65
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QY 66 AACCTGTCACTGCTCTTTCTCGAGCATGTCTTCATCAAGATGATGTTTAA 125
DB 68 AACACGTCACTGATCTCC-CTCGACCATGTCTTCATTAAGATGATGTTTAA 126
QY 126 GGAGAACTACAGGTGTGGAGAGTCCCTGTGTGGAGAGCATCAAGTGTCTGTT 185
DB 127 AGAAGACTGCGGAGTGTGAGTCTCAGATGGAGAGATGTCACACTCTGCTCTT 186
QY 186 TGTAGACATCTCTTCAAGACTGTCTGCCATGGATTCATACGAATGATGACGG 245
DB 187 TGTAGACATCTCTTCAAGAAAGGTTTCCCGTGGGATTCATCACAAAGCATACAGCG 246
QY 246 AGTTGGTGTAGAGCCCGCATGTCAGTGC-ATTGCAGTGTGAGAGGATGTTGC 304
DB 247 AGTGACCATGAGAGCCCGCATGCTCCTGCTTCCAGTCCGAGGCTATGTTGC 306
QY 305 CACCATGG 312
DB 307 CACCATGG 314

RESULT 12

AX409001

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

GENE LOGIC INC (US)

Location/Qualifiers

1..1356

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/note="EMBL/GenBank Accession No. D31815"
Best Local Similarity 76.0%; Pred. No. 9.4e-39;
Matches 234; Conservative 0; Mismatches 72; Indels 2; Gaps 2;

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DB 67 AACACGTCACTGATCTCC-CTCGACCATGTCTTCATTAAGATGATGTTTAA 126
QY 126 GGAGAACTACAGGTGTGGAGAGTCCCTGTGTGGAGAGGATCAAGTGTCTGTT 185
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DB 187 TGTAGACATCTCTTCAAGAAAGGTTTCCCGTGGAGATTCATCACAAAGTACAGCG 246
QY 246 AGTTGGTGTAGAGCCCGCATGTCAGTGC-ATTGCAGTGTGAGAGGATGTTGC 304
DB 247 AGTGACCATGAGAGCCCGCATGCTCCTGCTTCCAGTCCGAGGCTATGTTGC 306
QY 305 CACCATGG 312
DB 306 CACCATGG 313

RESULT 13

BD079930

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

LUDWIG INSTITUTE FOR CANCER RESEARCH

OS Homo sapiens (human)

PN JP 2001516009-A/596

PD 25-SEP-2001

PR 15-JUL-1998 JP 2000503425

PR 17-JUL-1997 US 08/896164,10-OCT-1997 US 60/061599 PR

10-OCT-1997 US 60/061765,10-OCT-1997 US 08/948705 PR

11-OCT-1997 GB 9721697.2,22-JUN-1998 US 09/102322 PI LLOYD

J OLD, MATTHEW J SCANLAN, ELISABETH STOCKERT, ALI GURE, YAO PI TSENG

CHEN, IVAN GOUT, MICHAEL O'HARE, YUICHI OBATA, MICHAEL PFREUNDSCHUH, PI

OZLEM TURECI, UGUR SAHIN

PI

GOIN33/574, A61K38/00, A61K39/395, A61K39/395, A61K45/00, A61K48/00, PC

A61P35/00, PC

C07K14/82, C07K16/32, C12N15/09//C07K16/46, C12P21/08, A61K37/02, PC

C12N18/00, CC

Cancer-associated nucleic acids and polypeptides. FH Key

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/mol_type="genomic DNA"

Location/Qualifiers

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 Matches 234; Conservative 0; Mismatches 72; Indels 2; Gaps 2;

QY 6 ACCCAGGTGAGTGTGAGTGTTCCTTTGCTCTTCAATTTAAAGATCTTGA AAAA 65
 Db 7 ACCAAGAGTGGAGGTGAGTGTCTCACTTTTGTCTTTTGAAGATCATTCGAGA 66
 QY 66 AACCTGTCACTGCTCTTTCCGCGACATGCTTCATCAATGATTAAGTCTTAA 125
 Db 67 AACACGTCACTGATCTCC-CCTGCGACCATGCTTCATTAAGATTGAGTGTTCGCC 125
 QY 126 GGAGAACTACAGGTGTGGGAGTCCCTGTGTGGAGAGGATCAAGTGTCTGCTT 185
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 Db 246 AGTGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 305
 QY 305 CACCATGG 312
 Db 306 CACCATGG 313

RESULT 14
 LOCUS E09013 1356 bp RNA linear PAT 29-SEP-1997
 DEFINITION CDNA encoding human-SMP30 protein.
 ACCESSION E09013
 VERSION E09013.1 GI:22025639
 KEYWORDS JP 1995097399-A/1.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Fukuyama, Y.; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 TITLE 1 (bases 1 to 1356)
 JOURNAL Fujita, K. and Maruyama, N.
 NEW POLYPEPTIDE AND REAGENT FOR MEASURING HUMAN SENSENCE MARKER
 PROTEIN SMP 30
 Patent: JP 1995097399-A 1 11-APR-1995;

JOURNAL
 FUJIREBIO INC

COMMENT
 OS Homo sapiens (Human)
 PN JP 1995097399-A/1
 PD 11-APR-1995
 PF 29-SEP-1993 JP 1993265681
 PI FUJITA KETKO, MARUYAMA NAOKI
 PC CORKI4/47, C12N15/09, C12Q1/68, G01N33/53, C07K99.00; CC
 strandedness: Double;
 CC topology: Linear;
 FH Key Location/Qualifiers
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BASE COUNT 373 a 274 c 343 g 366 t
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Query Match 54.1%; Score 168.8; DB 6; Length 1356;
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 Matches 234; Conservative 0; Mismatches 72; Indels 2; Gaps 2;

QY 6 ACCCAGGTGAGTGTGAGTGTTCCTTTGCTCTTCAATTTAAAGATCTTGA AAAA 65
 Db 7 ACCAAGAGTGGAGGTGAGTGTCTCACTTTTGTCTTTTGAAGATCATTCGAGA 66
 QY 66 AACCTGTCACTGCTCTTTCCGCGACATGCTTCATCAATGATTAAGTCTTAA 125
 Db 67 AACACGTCACTGATCTCC-CCTGCGACCATGCTTCATTAAGATTGAGTGTTCGCC 125
 QY 126 GGAGAACTACAGGTGTGGGAGTCCCTGTGTGGAGAGGATCAAGTGTCTGCTT 185
 Db 126 AAGAACTGCGGTGTGTGTGAGTCTCAGATGGAGAAAGTCCAACTCTGTCTT 185
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 QY 246 AGTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 304
 Db 246 AGTGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 305
 QY 305 CACCATGG 312
 Db 306 CACCATGG 313

RESULT 15
 LOCUS HUMSMP30 1356 bp mRNA linear PRI 07-FEB-1999
 DEFINITION Human mRNA for SMP-30 (senescence marker protein-30), complete cds.
 ACCESSION D31815
 VERSION D31815.1 GI:1072311
 KEYWORDS SMP-30; senescence marker protein-30.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Fukuyama, Y.; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 TITLE 1 (bases 1 to 1356)
 JOURNAL Maruyama, N.
 ISOLATION OF CDNA clone encoding human homologue of senescence
 marker protein-30 (SMP30) and its location on the X chromosome
 Biochim. Biophys. Acta 1263 (3), 249-252 (1995)
 PUBMED 7548213

REFERENCE
 AUTHORS Shirasawa, T.
 TITLE Direct Submission
 JOURNAL Submitted (11-JUN-1994) Takuji Shirasawa, Tokyo Metropolitan
 Institute of Gerontology, Molecular Pathology, 35-2 Sakae-cho,
 Itabashi-ku, Tokyo 173, JAPAN (Tel:813-3964-3241 (ex.3034),
 Fax:813-3579-4776)

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DHKIFVYIDSLSYSDAPDYDLOTGOISNRSVYKLEKEROI PDGMCIDAEGLWVAC
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BASE COUNT 994 .1356
ORIGIN

Query Match 54.1%; Score 168.8; DB 9; Length 1356;
Best Local Similarity 76.0%; Pred. No. 9,4e-39;
Matches 234; Conservative 0; Mismatches 72; Indels 2; Gaps 2;

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DB	7	ACCAAGAGTGAAGTCAAGTGTCTTGTCTTCTTGTGAAAGATCATTCGAGA	66
QY	66	AACCTGTCACTGTCTTTCTGCGACCATGTCTTCATCAAGATGATGTGTTAAG	125
DB	67	AACAGTCACTGATCTCC-CCTGCGACCATGTCTTCATTAAGATGAGTGTGTC	125
QY	126	GGAGACTAGAGTGTGGGAGTCCCTGTGTGGGAGAGGATCAAAGTGTCTGCTGT	185
DB	126	AGAGAACTGCCGGTGTGTGAGTCTCCAGTATGGAGAGTGTCCAACTCTGCTCTT	185
QY	186	TGTAGACATCCCTTCAAAAGACTGTCTGCGATGGGATTGCATCAGCAATCGAGTGCAGCG	245
DB	186	TGTAGACATTCCTGCAAAAAGTTGCCGTGGATTCATTCAACAGCAAGTACAGCG	245
QY	246	AGTTGTGTAGATGCCCGCACTCAATTGAGTGC-ATTGACAGTCAAGAGGCTATGTTGC	304
DB	246	AGTGACCATGATGCCCGCACTCAAGTCCGTGGCTCTTCGCCAGTCCGGAGGCTATGTTGC	305
QY	305	CACCATGG 312	
DB	306	CACCATTG 313	

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